

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

<120> Wuschel (WUS) Gene Homologs

<130> BB1410 PCT

<140>

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<150> 60/157216

<151> 1999-10-01

<160> 25

<170> Microsoft Office 97

<210> 1

<211> 462

<212> DNA

<213> Zea mays

<400> 1

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tcttgacgga gctcttcgcg gcggggctgc ggacgcccag cacggagcag attcagcgca 360
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<210> 2

<211> 77

<212> PRT

<213> Zea mays

<400> 2

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Met Glu Ala Leu Ser Gly Arg Val Gly Val Lys Cys Gly Arg Trp Asn
  1             5             10             15

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Pro Thr Ala Glu Gln Val Lys Val Leu Thr Glu Leu Phe Arg Ala Gly
      20             25             30

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Leu Arg Thr Pro Ser Thr Glu Gln Ile Gln Arg Ile Ser Asn Gln Leu
      35             40             45

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Ser Ala Phe Gly Lys Gly Glu Asn Lys Asn Val Leu Leu Thr Gly Pro
      50             55             60

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Lys Gln Lys Gly Arg Glu Arg Gln Gln Gln Lys Lys Arg
      65             70             75

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<210> 3

<211> 1338

<212> DNA

<213> Zea mays

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aaccacacat atagctgaag caaatatata cacttgctta actggcggtg tagtgtagct 180
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<210> 4
<211> 220
<212> PRT
<213> Zea mays

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<400> 4
Met Glu Ala Leu Ser Gly Arg Val Gly Val Lys Cys Gly Arg Trp Asn
  1             5             10             15

Pro Thr Ala Glu Gln Val Lys Val Leu Thr Glu Leu Phe Arg Ala Gly
      20             25             30

Leu Arg Thr Pro Ser Thr Glu Gln Ile Gln Arg Ile Ser Thr His Leu
  35             40             45

Ser Ala Phe Gly Lys Val Glu Ser Lys Asn Val Phe Tyr Trp Phe Gln
  50             55             60

Asn His Lys Ala Arg Glu Arg His His His Lys Lys Arg Arg Arg Gly
  65             70             75             80

Ala Ser Ser Ser Ser Pro Asp Ser Gly Ser Gly Arg Gly Ser Asn Asn
      85             90             95

Glu Glu Asp Gly Arg Gly Ala Ala Ser Gln Ser His Asp Ala Asp Ala
  100             105             110

Asp Ala Asp Leu Val Leu Gln Pro Pro Glu Ser Lys Arg Glu Ala Arg
  115             120             125

Ser Tyr Gly His His His Arg Leu Val Thr Cys Tyr Val Arg Asp Val
  130             135             140

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Val Glu Gln Gln Glu Ala Ser Pro Ser Trp Glu Arg Pro Thr Arg Glu
 145 150 155 160

Val Glu Thr Leu Glu Leu Phe Pro Leu Lys Ser Tyr Gly Asp Leu Glu
 165 170 175

Ala Ala Glu Lys Val Arg Ser Tyr Val Arg Gly Ile Ala Ala Thr Ser
 180 185 190

Glu Gln Cys Arg Glu Leu Ser Phe Phe Asp Val Ser Ala Gly Arg Asp
 195 200 205

Pro Pro Leu Glu Leu Arg Leu Cys Ser Phe Gly Pro
 210 215 220

<210> 5
 <211> 720
 <212> DNA
 <213> Zea mays

<400> 5
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 gtatatataa ctgttaggta cggcggtgcg cgcccgccag actacatggg cgtgacggac 660
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<210> 6
 <211> 238
 <212> PRT
 <213> Zea mays

<400> 6
 Met Ala Ala Asn Ala Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Ser
 1 5 10 15

Gly Ser Val Ala Ala Pro Ala Val Cys Arg Pro Ser Gly Ser Arg Trp
 20 25 30

Thr Pro Thr Pro Glu Gln Ile Arg Met Leu Lys Glu Leu Tyr Tyr Gly
 35 40 45

Cys Gly Ile Arg Ser Pro Ser Ser Glu Gln Ile Gln Arg Ile Thr Ala
 50 55 60

Met Leu Arg Gln His Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp
 65 70 75 80

Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Arg Arg Leu Thr Ser
 85 90 95

Leu Asp Val Asn Val Pro Ala Ala Gly Ala Ala Asp Ala Thr Thr Ser
 100 105 110
 Gln Leu Gly Val Leu Ser Leu Ser Ser Pro Pro Pro Ser Gly Ala Ala
 115 120 125
 Pro Pro Ser Pro Thr Leu Gly Leu Tyr Ala Ala Gly Asn Gly Gly Gly
 130 135 140
 Ser Ala Val Leu Leu Asp Thr Ser Ser Asp Trp Gly Ser Ser Gly Ala
 145 150 155 160
 Ala Met Ala Thr Glu Thr Cys Phe Leu Gln Val Gly Ala Val Val Arg
 165 170 175
 Ser Phe Leu Gly His Cys Ala Gln Phe His Val Arg Thr Tyr Glu Leu
 180 185 190
 Ile Ala Ala Ser Phe His Pro Pro Val Tyr Ile Thr Val Arg Tyr Gly
 195 200 205
 Gly Ala Arg Pro Gln Asp Tyr Met Gly Val Thr Asp Thr Gly Ser Ser
 210 215 220
 Ser Gln Trp Pro Arg Phe Ser Ser Ser Asp Thr Ile Met Ala
 225 230 235

<210> 7
 <211> 767
 <212> DNA
 <213> Zea mays

<400> 7
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 cgccgcgggc gcggccgacg ccaccaccag ccaactcggc gtcctctcgc tgtcgtcgcc 420
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 tataactgtt aggtacggcg gtgcgcgccc gcaggactac atgggcgtga cggacacggg 720
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<210> 8
 <211> 237
 <212> PRT
 <213> Zea mays

<400> 8
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 20 25 30

<210> 9
<211> 1367
<212> DNA
<213> Zea mays

<400>	9						
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cccgcatttc	ccagccttca	gtagcagcag	cagtacgtcg	cgccctgccc	atcgatccat		180
ctggctatca	tacctgcctga	catggaaggc	ggactgagcc	cggagcggga	cgcgggcggg		240
gagccggtgc	ggtcgcggtg	gagcccaag	ccggagcaga	tactcatcct	cgagtcctac		300
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ggatcgcccc	ccacgagcgg	cctcgcaacc	ggacacgcga	cggcttcgtc	gacggcgggg		540
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tccgcgcaga	tgggtctacg	cagcggcggt	ggctccggct	ccgcgtcctc	ggcggcgcgc		720
gccaccacag	agcagcagca	gcagctttac	tactcgccgt	gccagccagc	gagcatgacg		780

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cacacaaaca aatagagtgt tgtacctacg acgcatccac atcgaacatc tataactaagt 1320
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<210> 10

<211> 253

<212> PRT

<213> Zea mays

<400> 10

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Met Glu Gly Gly Leu Ser Pro Glu Arg His Ala Ala Ala Glu Pro Val
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Arg Ser Arg Trp Thr Pro Lys Pro Glu Gln Ile Leu Ile Leu Glu Ser
      20              25              30

```

```

Ile Phe Asn Ser Gly Met Val Asn Pro Pro Lys Asp Glu Thr Val Arg
      35              40              45

```

```

Ile Arg Lys Leu Leu Glu Arg Phe Gly Ala Val Gly Asp Ala Asn Val
      50              55              60

```

```

Phe Tyr Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg Gln Arg
      65              70              75              80

```

```

Gln Leu Gln Ala Gln Ala Ala Ala Ser Ser Ser Ser Ser Gly Ser Pro
      85              90              95

```

```

Pro Thr Ser Gly Leu Ala Pro Gly His Ala Thr Ala Ser Ser Thr Ala
      100             105             110

```

```

Gly Met Phe Ala His Gly Ala Thr Tyr Gly Ser Ser Ala Ser Ala Ser
      115             120             125

```

```

Trp Pro Pro Pro Pro Ser Cys Glu Gly Met Met Gly Asp Leu Asp Tyr
      130             135             140

```

```

Gly Gly Gly Asp Asp Leu Phe Ala Ile Ser Arg Gln Met Gly Tyr Ala
      145             150             155             160

```

```

Ser Gly Gly Gly Ser Gly Ser Ala Ser Ser Ala Ala Val Ala His His
      165             170             175

```

```

Glu Gln Gln Gln Gln Leu Tyr Tyr Ser Pro Cys Gln Pro Ala Ser Met
      180             185             190

```

```

Thr Val Phe Ile Asn Gly Val Ala Thr Glu Val Pro Arg Gly Pro Ile
      195             200             205

```

```

Asp Leu Arg Ser Met Phe Gly Gln Asp Val Met Leu Val His Ser Thr
      210             215             220

```

Ala Gly Leu Leu Pro Val Asn Glu Tyr Gly Val Leu Thr Gln Ser Leu
 225 230 235 240

Gln Met Gly Glu Ser Tyr Phe Leu Val Thr Arg Gly Tyr
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<210> 11
 <211> 513
 <212> DNA
 <213> Zea mays

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gcccgcgaat accgatgccg attggcgccg ccgccgcccg ctngcattgc aaacgaacaa 360
cngggggngc gcgtttttat cttacangaa acccattcta ctttgctgcc ccgcaagggc 420
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<210> 12

<211> 89

<212> PRT

<213> Zea mays

<220>

<221> UNSURE

<222> (53)

<220>

<221> UNSURE

<222> (55)

<400> 12

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Gln Val Ala Val Leu Glu Gly Leu Tyr Glu His Gly Leu Arg Thr Pro
 1              5              10              15

Ser Ala Glu Gln Ile Gln Gln Ile Thr Gly Arg Leu Arg Glu His Gly
          20              25              30

Ala Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala
          35              40              45

Arg Gln Arg Gln Xaa Gln Xaa Ala Gly Gln Leu Arg Leu Leu Gln Gln
 50              55              60

Ala Pro Pro Pro Ala Pro Ala Ala Ala Arg Ala Leu His Ala Pro Arg
 65              70              75              80

Ala Thr Val Pro Ser Arg Pro Arg Pro
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<210> 13

<211> 1194

<212> DNA

<213> Zea mays

<400> 13

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ccagcgcagc aggcagaagc aggacagctt cgctacttc agcaggctcc tccgcgggcc 240
cccgcgcgtg cccgtgctct ccatgcccc cgcgccaccg taccatcacg cccgcgtccc 300

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ggcgccgccc gcgataccga tgccgatggc gccgcccgcg cccgctgcat gcaacgacaa 360
cggcgccgcg cgtgtgatct acaggaaccc attctacgtg gctgcgccgc aggcgcccc 420
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cagccgcgag acgctccagc tgttcccgc tccagccac cttcgtgctg cggcacgaca 660
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaag 1194

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<210> 14

<211> 221

<212> PRT

<213> Zea mays

<400> 14

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Trp Ala Thr Lys Glu Gln Val Ala Val Leu Glu Gly Leu Tyr Glu His
  1              5              10              15

Gly Leu Arg Thr Pro Ser Ala Glu Gln Ile Gln Gln Ile Thr Gly Arg
      20              25              30

Leu Arg Glu His Gly Ala Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe
      35              40              45

Gln Asn His Lys Ala Arg Gln Arg Gln Arg Gln Lys Gln Asp Ser Phe
      50              55              60

Ala Tyr Phe Ser Arg Leu Leu Arg Arg Pro Pro Pro Leu Pro Val Leu
      65              70              75              80

Ser Met Pro Pro Ala Pro Pro Tyr His His Ala Arg Val Pro Ala Pro
      85              90              95

Pro Ala Ile Pro Met Pro Met Ala Pro Pro Pro Pro Ala Ala Cys Asn
      100             105             110

Asp Asn Gly Gly Ala Arg Val Ile Tyr Arg Asn Pro Phe Tyr Val Ala
      115             120             125

Ala Pro Gln Ala Pro Pro Ala Asn Ala Ala Tyr Tyr Tyr Pro Gln Pro
      130             135             140

Gln Gln Gln Gln Gln Gln Gln Val Thr Val Met Tyr Gln Tyr Pro Arg
      145             150             155             160

Met Glu Val Ala Gly Gln Asp Lys Met Met Thr Arg Ala Ala Ala His
      165             170             175

Gln Gln Gln Gln His Asn Gly Ala Gly Gln Gln Pro Gly Arg Ala Gly
      180             185             190

```

His Pro Ser Arg Glu Thr Leu Gln Leu Phe Pro Pro Pro Ala His Leu
 195 200 205

Arg Ala Ala Ala Arg Gln Gly Ala Arg Arg Gln Arg Gln
 210 215 220

<210> 15
 <211> 506
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (19)

<220>
 <221> unsure
 <222> (489)..(490)

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 tagacatggt ggagaacttt tacaagcagg gaataaggac tcccagcact gagcaaatac 180
 aacagattac ctctaggctt agggccttatg gttacatcga gggaaaaaat gtcttctact 240
 ggttttcaaaa tcacaaagcg cgccaaagac agaagctcaa gcagaagcaa caaagcattg 300
 catactgcaa ttgcttttctt catgcctccc accccatttg ccaaaatggt gtctgcgtcc 360
 atattgtttg caaaagagtg gattcagctt ttatcctcac caaccaaagg tgcttgcaag 420
 tgtagggtatt agctcaaggg attgagactg ggtccttttg catgctaaag aatatgtgat 480
 ggcattgcann agtgaacacc cggatt 506

<210> 16
 <211> 134
 <212> PRT
 <213> Glycine max

<400> 16
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 Ser Ser Gly Ala His Ser Ser Val Ser Arg Trp Ser Pro Thr Lys Glu
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 Gln Ile Asp Met Leu Glu Asn Phe Tyr Lys Gln Gly Ile Arg Thr Pro
 35 40 45
 Ser Thr Glu Gln Ile Gln Gln Ile Thr Ser Arg Leu Arg Ala Tyr Gly
 50 55 60
 Tyr Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala
 65 70 75 80
 Arg Gln Arg Gln Lys Leu Lys Gln Lys Gln Gln Ser Ile Ala Tyr Cys
 85 90 95
 Asn Cys Phe Leu His Ala Ser His Pro Ile Cys Gln Asn Val Val Cys
 100 105 110

Val His Ile Val Cys Lys Arg Val Asp Ser Ala Phe Ile Leu Thr Asn
 115 120 125

Gln Arg Cys Leu Gln Val
 130

<210> 17
 <211> 844
 <212> DNA
 <213> Glycine max

<400> 17
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 caagcagggga ataaggactc ccagcactga gcaaatacaa cagattacct ctaggcttag 180
 ggcttatggt tacatcgagg gaaaaaatgt cttctactgg tttcaaaatc acaaagcgcg 240
 ccaaagacag aagctcaagc agaagcaaca aagcattgca tactgcaatt gctttcttca 300
 tgccctccac cccatttgcc aaaatgttgt ctgcgctcca tattgtttgc aaaagagtgg 360
 attcagcttt tatcctcacc aaccaaaggt gcttgcaagt gtaggtatta gctcaaggat 420
 tgagactggg tcctttggca tgctaagaat atgtgatggc atgcagagtg aacacccgga 480
 ttataactat agcaccagta accgtgaagc cttaactcta tttcctcttc atccaaccgg 540
 tattttggaa gaaaaaaciaa ctcacactc tggtgatgtc accgacaaat cttttgtttc 600
 tattgctgtt gacgaaaatg gtcaccttgg aaatcaacc tgctttaatt ttcagtactg 660
 aagaacgaag gtatcgagat agtgattaag tatcatcgac caaaactact aacactgtac 720
 tactactttc tttgagtagc tcgttggttca tcttcgaaat gagttttatc taattggata 780
 ttgagtttaa cgtagtataa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840
 aaaa 844

<210> 18
 <211> 217
 <212> PRT
 <213> Glycine max

<400> 18
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 1 5 10 15
 Ala His Ser Ser Val Ser Arg Trp Ser Pro Thr Lys Glu Gln Ile Asp
 20 25 30
 Met Leu Glu Asn Phe Tyr Lys Gln Gly Ile Arg Thr Pro Ser Thr Glu
 35 40 45
 Gln Ile Gln Gln Ile Thr Ser Arg Leu Arg Ala Tyr Gly Tyr Ile Glu
 50 55 60
 Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Gln Arg
 65 70 75 80
 Gln Lys Leu Lys Gln Lys Gln Gln Ser Ile Ala Tyr Cys Asn Cys Phe
 85 90 95
 Leu His Ala Ser His Pro Ile Cys Gln Asn Val Val Cys Ala Pro Tyr
 100 105 110
 Cys Leu Gln Lys Ser Gly Phe Ser Phe Tyr Pro His Gln Pro Lys Val
 115 120 125

Leu Ala Ser Val Gly Ile Ser Ser Arg Ile Glu Thr Gly Ser Phe Gly
 130 135 140

Met Leu Arg Ile Cys Asp Gly Met Gln Ser Glu His Pro Asp Tyr Asn
 145 150 155 160

Tyr Ser Thr Ser Asn Arg Glu Ala Leu Thr Leu Phe Pro Leu His Pro
 165 170 175

Thr Gly Ile Leu Glu Glu Lys Thr Thr His His Ser Val Asp Val Thr
 180 185 190

Asp Lys Ser Phe Val Ser Ile Ala Val Asp Glu Asn Gly His Leu Gly
 195 200 205

Asn Gln Pro Cys Phe Asn Phe Gln Tyr
 210 215

<210> 19

<211> 741

<212> DNA

<213> Glycine max

<400> 19

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atgtaaggac tcattcatca gtttcacggg ggagtcctac aaaggagcaa atagacatgt 120
tagagaacct ttacaagcag ggaataagga ctccagcac tgagcaaata caacagatta 180
cctctaggct cagggcttat ggtcacatcg agggaaagaa tgtcttctac tggtttcaaa 240
atcacaaagc tcgtcaaaga cagaagctga tgaagcaaca aaccattgca tattccaatc 300
gctttcttcg tgcctcccac cccatttgcc aaaatgttgc ctgcgctcca tattgtttgc 360
aacggagtggt attcagcttt tatectcaac aatcgaaggt gcttgcaagt ggaggtataa 420
gttcaactgg gccttttaggc atgcaaagaa tgtttgatgg catgcagagt agtgaacacc 480
cggattgtaa ccgtgaagtc ttaactctct ttcctcttca tccaaccggc attttgaaag 540
aaaaaacaac tcatcaagtg ccttccttgg ctccaacttc tgttggtgct gttgatgaag 600
atggtcacatc tggaaatcag cccttcttta attttttcac tactgaacca aggtcgagag 660
agtgattagg tggttaattgt cattgaccaa aaaaacaact aacatggcac tactttgagt 720
aaaaaaaaaa aaaaaaaaaa a
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<210> 20

<211> 212

<212> PRT

<213> Glycine max

<400> 20

Met Glu Ser His Ser Ser Asp Ala Glu Ala Glu Asn Val Arg Thr His
 1 5 10 15

Ser Ser Val Ser Arg Trp Ser Pro Thr Lys Glu Gln Ile Asp Met Leu
 20 25 30

Glu Asn Leu Tyr Lys Gln Gly Ile Arg Thr Pro Ser Thr Glu Gln Ile
 35 40 45

Gln Gln Ile Thr Ser Arg Leu Arg Ala Tyr Gly His Ile Glu Gly Lys
 50 55 60

Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Gln Arg Gln Lys
 65 70 75 80

Leu	Met	Lys	Gln	Gln	Thr	Ile	Ala	Tyr	Ser	Asn	Arg	Phe	Leu	Arg	Ala	
				85					90					95		
Ser	His	Pro	Ile	Cys	Gln	Asn	Val	Ala	Cys	Ala	Pro	Tyr	Cys	Leu	Gln	
				100					105					110		
Arg	Ser	Gly	Phe	Ser	Phe	Tyr	Pro	Gln	Gln	Ser	Lys	Val	Leu	Ala	Ser	
				115					120					125		
Gly	Gly	Ile	Ser	Ser	Thr	Gly	Pro	Leu	Gly	Met	Gln	Arg	Met	Phe	Asp	
				130					135					140		
Gly	Met	Gln	Ser	Ser	Glu	His	Pro	Asp	Cys	Asn	Arg	Glu	Val	Leu	Thr	
				145					150					155		
Leu	Phe	Pro	Leu	His	Pro	Thr	Gly	Ile	Leu	Lys	Glu	Lys	Thr	Thr	His	
				165					170					175		
Gln	Val	Pro	Ser	Leu	Ala	Ser	Thr	Ser	Val	Val	Ala	Val	Asp	Glu	Asp	
				180					185					190		
Gly	His	Leu	Gly	Asn	Gln	Pro	Phe	Phe	Asn	Phe	Phe	Thr	Thr	Glu	Pro	
				195					200					205		
Arg	Ser	Arg	Glu													
				210												

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<210> 21
<211> 906
<212> DNA
<213> Glycine max
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acaccatttc	tccacctcat	catcctgtta	caaccttcga	cctcaagagc	ttcatcaaac	180
ctgaaagtgc	ctccagaaaa	cttggaattg	gatcctccga	tgataatact	aataagagag	240
acccatcttc	accccagggc	caggctgaaa	cgcatattcc	aggagggaca	cggtggaatc	300
cgactcaaga	acaaataggg	atatttggaga	tgctgtacag	aggagggatg	cgaactccga	360
atgctcaaca	aatagagcag	atcacagcac	agcttagcaa	gtacggcgaag	atcgaaggga	420
agaacgtggt	ctattgggtc	caaaaccaca	aagcacgcga	gagacagaag	cagaagcgta	480
acaacytagg	ccttgctcat	agtctctgta	ctactctcac	cacttcaccc	ccctttagtt	540
gttgtgtaat	taccactatg	gacaccacaa	aacgggggga	agtagtagaa	agagaggagg	600
aagatagccc	gttgaagaag	tgtaggagct	gggcgtttga	gtacttgga	gaccaaagag	660
aggaggaaca	tagaactctg	gagcttttcc	cattgcaccc	ggaaggcaga	tgaaggggtt	720
tgttttaatt	gtttgaccaa	tttaacgaga	aatattttta	gcttttaatt	aattgtttct	780
gaacctctca	ggctgattgg	aatgtatgtg	ctttaattag	tttggtttag	tttttcatca	840
ccttcttctt	tggttggtgt	gggaaagaag	aaaacacaaa	gtcgtctaca	aaaaaaaaaa	900
aaaaaa						906

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<210> 22
<211> 231
<212> PRT
<213> Glycine max
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<400> 22

Met Lys Val His Gln Phe Ala Arg Gly Phe Trp Glu His Glu Pro Ser
 1 5 10 15

Leu Thr Leu Gly Cys Lys Arg Leu Arg Pro Leu Ala Pro Lys Leu Ser
 20 25 30

Asn Thr Asp Thr Ile Ser Pro Pro His His Pro Val Thr Thr Phe Asp
 35 40 45

Leu Lys Ser Phe Ile Lys Pro Glu Ser Ala Ser Arg Lys Leu Gly Ile
 50 55 60

Gly Ser Ser Asp Asp Asn Thr Asn Lys Arg Asp Pro Ser Ser Pro Gln
 65 70 75 80

Gly Gln Ala Glu Thr His Ile Pro Gly Gly Thr Arg Trp Asn Pro Thr
 85 90 95

Gln Glu Gln Ile Gly Ile Leu Glu Met Leu Tyr Arg Gly Gly Met Arg
 100 105 110

Thr Pro Asn Ala Gln Gln Ile Glu Gln Ile Thr Ala Gln Leu Ser Lys
 115 120 125

Tyr Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His
 130 135 140

Lys Ala Arg Glu Arg Gln Lys Gln Lys Arg Asn Asn Leu Gly Leu Ala
 145 150 155 160

His Ser Pro Arg Thr Thr Leu Thr Thr Ser Pro Pro Phe Ser Cys Cys
 165 170 175

Val Ile Thr Thr Met Asp Thr Thr Lys Arg Gly Glu Val Val Glu Arg
 180 185 190

Glu Glu Glu Asp Ser Pro Leu Lys Lys Cys Arg Ser Trp Ala Phe Glu
 195 200 205

Tyr Leu Glu Asp Gln Arg Glu Glu Glu His Arg Thr Leu Glu Leu Phe
 210 215 220

Pro Leu His Pro Glu Gly Arg
 225 230

<210> 23

<211> 904

<212> DNA

<213> Glycine max

<400> 23

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 taccctttc gatctcaaga gtttcatcag gcccgaaagt ggccccagaa aaccggttc 180
 ctctgacgac actaagaagg atccaccttc accccaaggc cagattgaaa cgcacccagg 240
 agggacacgg tggaatccta cgcaagaaca gataggcata ttggagatgt tgtacaaagg 300
 agggatgcga actccgaatg ctcaacagat agagcagatc actgtccagc ttggaaagta 360
 cggcaagatc gaagggaaga acgtgttcta ttggtttcag aatcacaaag cacgcgagag 420

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acaaaagcag aagcgcagca gccttgcac ttctcatagt cctcgaactc ccacaattca 480
cagtgttggt actttggaga caacaagggg ggaagtggta gagagagatc acgaggaaga 540
tagtccgtac aagaagaagt gcaggagatg ggtatttgac tgcttggaag aacaaaacat 600
gtcatcacct tgtgaacaag aggaacatag aactctggag ctttttccat tgcacccgga 660
aggcagatga aggggtttga gtttgattga ccatattatct atcatttttc actttgcttt 720
agttccgaat cgcagctgat tattgaatga atgtggttta attaatttgc tttacttttc 780
ttttttcttt gtattgggaa agaagaaaga caaagttgtc tctgatctgt actcttcac 840
ttaatgctat tcctgacttt ggaacccaaa aaaaaaaaaa aaaactcgga gagagcgaac 900
tagt                                     904

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<210> 24

<211> 221

<212> PRT

<213> Glycine max

<400> 24

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Met Lys Val His Gln Phe Thr Arg Gly Leu Ile Trp Glu His Glu Pro
  1                      5                      10                      15

Phe Leu Thr Leu Gly Cys Lys Arg Leu Arg Pro Leu Ala Pro Lys Leu
          20                      25                      30

Pro Asn Thr Lys Thr Ile Thr Thr Pro Phe Asp Leu Lys Ser Phe Ile
          35                      40                      45

Arg Pro Glu Ser Gly Pro Arg Lys Pro Val Ser Ser Asp Asp Thr Lys
          50                      55                      60

Lys Asp Pro Pro Ser Pro Gln Gly Gln Ile Glu Thr His Pro Gly Gly
          65                      70                      75                      80

Thr Arg Trp Asn Pro Thr Gln Glu Gln Ile Gly Ile Leu Glu Met Leu
          85                      90                      95

Tyr Lys Gly Gly Met Arg Thr Pro Asn Ala Gln Gln Ile Glu Gln Ile
          100                      105                      110

Thr Val Gln Leu Gly Lys Tyr Gly Lys Ile Glu Gly Lys Asn Val Phe
          115                      120                      125

Tyr Trp Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Gln Lys Arg
          130                      135                      140

Ser Ser Leu Ala Ser Ser His Ser Pro Arg Thr Pro Thr Ile His Ser
          145                      150                      155                      160

Val Val Thr Leu Glu Thr Thr Arg Gly Glu Val Val Glu Arg Asp His
          165                      170                      175

Glu Glu Asp Ser Pro Tyr Lys Lys Lys Cys Arg Arg Trp Val Phe Asp
          180                      185                      190

Cys Leu Glu Glu Gln Asn Met Ser Ser Pro Cys Glu Gln Glu Glu His
          195                      200                      205

Arg Thr Leu Glu Leu Phe Pro Leu His Pro Glu Gly Arg
          210                      215                      220

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<210> 25
 <211> 291
 <212> PRT
 <213> Arabidopsis thaliana

<400> 25

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Met Glu Pro Pro Gln His Gln His His His His Gln Ala Asp Gln Glu
 1          5          10          15

Ser Gly Asn Asn Asn Asn Lys Ser Gly Ser Gly Gly Tyr Thr Cys Arg
          20          25          30

Gln Thr Ser Thr Arg Trp Thr Pro Thr Thr Glu Gln Ile Lys Ile Leu
          35          40          45

Lys Glu Leu Tyr Tyr Asn Asn Ala Ile Arg Ser Pro Thr Ala Asp Gln
          50          55          60

Ile Gln Lys Ile Thr Ala Arg Leu Arg Gln Phe Gly Lys Ile Glu Gly
          65          70          75          80

Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Glu Arg Gln
          85          90          95

Lys Lys Arg Phe Asn Gly Thr Asn Met Thr Thr Pro Ser Ser Ser Pro
          100          105          110

Asn Ser Val Met Met Ala Ala Asn Asp His Tyr His Pro Leu Leu His
          115          120          125

His His His Gly Val Pro Met Gln Arg Pro Ala Asn Ser Val Asn Val
          130          135          140

Lys Leu Asn Gln Asp His His Leu Tyr His His Asn Lys Pro Tyr Pro
          145          150          155          160

Ser Phe Asn Asn Gly Asn Leu Asn His Ala Ser Ser Gly Thr Glu Cys
          165          170          175

Gly Val Val Asn Ala Ser Asn Gly Tyr Met Ser Ser His Val Tyr Gly
          180          185          190

Ser Met Glu Gln Asp Cys Ser Met Asn Tyr Asn Asn Val Gly Gly Gly
          195          200          205

Trp Ala Asn Met Asp His His Tyr Ser Ser Ala Pro Tyr Asn Phe Phe
          210          215          220

Asp Arg Ala Lys Pro Leu Phe Gly Leu Glu Gly His Gln Asp Glu Glu
          225          230          235          240

Glu Cys Gly Gly Asp Ala Tyr Leu Glu His Arg Arg Thr Leu Pro Leu
          245          250          255

Phe Pro Met His Gly Glu Asp His Ile Asn Gly Gly Ser Gly Ala Ile
          260          265          270

Trp Lys Tyr Gly Gln Ser Glu Val Arg Pro Cys Ala Ser Leu Glu Leu
          275          280          285

```


Arg Leu Asn
290

FIGURE 1

```

*      *      *      *      *      *      *      *      *      *      *
MEALS-----
MEG-----GLSPERHAAE-----
MESH-----
MKVHQFARGF-WEHEPSLTGLCKRLRPLAPKLSNTDTISPPHPVTTFDLKSFIKPESAS
MKVHQFTRGLIWEHEPFLTGLCKRLRPLAPKLPNTKTITP-----FDLKSFIROPESGP
MEPPQHQH-----HHH-----
1
60

**      *      *      *      *      *      *      *      *
-----G-----RVGK-----GRWNPTAEQVKVLTFL-RAGLRTPSTEQ
-----PVRSRWTPKPEQILILEIF-NSGMVNPPEKDE
-----SDAEAEVNRTHSSV-----SRWSPTEQIDMLENLY-KQGIRTPSTEQ
RKLIGSSDDNTNKRDPSSPQQAETHIPGGTRWNPTQEQIGILEMLY-RGGMRTPNAAQQ
RK-----PVSSDDTKKDPSPQEQIETH-PGGTRWNPTQEQIGILEMLY-KGGMRTPNAAQQ
-----QADQESGNNNNKSGGGYTCR-QTSTRWTPTEQIKILKELYNNNAIRSPTADQ
61
120

*      *      *      *      *      *      *      *      *      *      *
IQRISTHLSAFGKVESKNVYWFQNHKARERHHK-KRRRGASSSPDSGSGRGSNNEED
TVRIRKLLERFAGVDANVYWFQNRRRSRRRRQRLQAQAAASSSSGSPPTSGLAPGH
IQQITSRRLRAYGHIEGKNVYWFQNHKARQKLM-KQQTIAYSNR-----FLRASHPICQ
IEQITAQLSKYKIEGKNVYWFQNHKARERQKQ--KRNNLGLAHSPTTLTSPPFSC-
IEQITVQLGKYKIEGKNVYWFQNHKARERQKQ--KRSSLASSHSPTPTIHS-----
IQKITARLRQFGKIEGKNVYWFQNHKARERQKRRKENGNTMTTPSSSPNSVMMAANDHYH
121
180
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SEQ ID NO:04
SEQ ID NO:10
SEQ ID NO:20
SEQ ID NO:22
SEQ ID NO:24
SEQ ID NO:25

SEQ ID NO:04
SEQ ID NO:10
SEQ ID NO:20
SEQ ID NO:22
SEQ ID NO:24
SEQ ID NO:25

SEQ ID NO:04
SEQ ID NO:10
SEQ ID NO:20
SEQ ID NO:22
SEQ ID NO:24
SEQ ID NO:25
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FIGURE 1 CONTINUED

SEQ ID NO:04	---GRGAASQSHDAD-ADADLVLPPEKREARS-YG--HHRL-----	* *
SEQ ID NO:10	ATASSTAGMFAHGATYGSSASASWPPPPSCGMMGDLDDYGGDDDLFAISRQMGYASGGGS	
SEQ ID NO:20	---NVACAPYCLQ---RSGFSFYPPQSKVLASGGIS--STGPL-----	
SEQ ID NO:22	-----CVITTMDDT-KRGEVV---ERE-EEDSPLK--K-CR-----	
SEQ ID NO:24	-----VVTLETT--RGEVV---ERDHEEDSPYK--KKCR-----	
SEQ ID NO:25	PLHHHHGVPMQORPA-NSVNVKLNQDHHLYHHNKPYPSPFNNGNLNHASSGTECGVVNASN	
	181	240
	*	*
SEQ ID NO:04	--VTCYVRDVVEQQ-----EASPSWERTRE-----VETLEFPLKSYGDLE--A	
SEQ ID NO:10	GSASSAAVAHHEQQOQLYSP-----COPASMTVFINGVATEVPRGPIDLRSMF	
SEQ ID NO:20	--G---MQRMFDGM-----QSS---EHPDCN-----REVLTFLPLHPTGILKEKT	
SEQ ID NO:22	----SWAFEYLEDQ-----R-----EE--E-----HRTLEFPLHPEG-----	
SEQ ID NO:24	----RWVFDCLLEQ-----NMSSPCEQE--E-----HRTLEFPLHPEG-----	
SEQ ID NO:25	GYMSSHVYGSMEQDCSMNYYNNVGGWANMDHHYSSAPYNFFDRAKPLFEGLEGHQDEEECG	
	241	300
	*	*
SEQ ID NO:04	AEKVRSYVRGIA---ATS---EQCRELS---FFDVSAGRDP--LELRCSFGP	**** *
SEQ ID NO:10	GQDVMLVHSTAGLLPVNEYGVLTQSLQMGESYF-----LVTRGY	
SEQ ID NO:20	THQVPSLASTSV---VAV---DEDGHLGNQPFNFTEPR--RE-----	
SEQ ID NO:22	-----R-----	
SEQ ID NO:24	-----R-----	
SEQ ID NO:25	GDAYLEHRRRTLPLFPMHG---EDHINGSGGAIWKYGQSEVRPCASLELRL---N	
	301	356